In the specification:

Please amend the paragraph beginning at page **10**, line **27** as follows:

Arabidopsis plants expressing DNA methyltransferase 1 (Met1) antisense (Met 1as) gene contain reduced levels of DNA methyltransferase activity and a correspondingly reduced level of general DNA methylation (Finnegan et al., ~~1995~~ 1996; Ronemus et al., 1996). In contrast to *ddm* mutants, *Arabidopsis* plants expressing a Met1 as gene develop various developmental abnormalities at high frequency and without repeated self-fertilization, including floral abnormalities (Finnegan et al., 1996). PCT/US971/13358 also reports that *Arabidopsis* plants expressing a Met1 as gene alter the rate of development of the plant. The development of the endosperm in *ddm* mutants and plants expressing Met1as has not been reported.

Please amend the paragraph at page **18**, line **17** as follows:

i)Methylase 1 (acc. nr.[-] LC10692;

Please amend Table 1 at pages **25-26**, rows **8-9**, **11** and **13**, and at footnote **8** as follows:

Table 1. Outcomes of control crosses and crosses involving Met1 antisense and *ddm* mutant plants.

Cross	Interploidy cross phenotype[1]	Viability of hybrid see (%)[2]	Maximum number of peripheral endosperm nuclei[3]	Relative volume of chalazal endosperm[4]	Relative change to cellularization time (days)[5]	Seed weight (µg)[6]
2x-2x	NA	95-100	400	1	0	22
4x-4x	NA	95-100	400	2.5	0	36
6x-6x	NA	95-100	300	3.5	0	44
2x-4x	PE	95-100	640	2	+1	54
4x-2x	ME	95-100	80	0.6	-1	14
2x-6x	PE	0[7]	400	6.8	Absent	6
6x-2x	ME	0[7]	50	0.2	-1.5	4
2xmet-2xmet	PE	95-100	350	1	0	15
2xmet-2xmet		(90)[8]	(598)[8]			(13.6)[8]
2x-2xmet	ME	95-100	200	0.5	-0.5	10
2x~~met~~-2xmet		(93)[8]	(227)[8]			(9.5)[8]
2xmet-2x	PE	95-100	450	1.75	+0.5	20
2xmet-2x~~m~~		(97)[8]	(1,365)[8]			(32.5)[8]

2xddm-2xddm	PE	95-100	350	1.25	0	19
2x-2xddm	ME	95-100	250	0.5	-0.5	12
2xddm-2x	PE	95-100	400	2	+0.5	21
4x-2xmet	ME	0[7]	740	4.4	>+3	15
4x-2xddm	ME	0[7]	150	0.3	-1.5	5
2xddm-4x	PE	0[7]	680	3.5	>+3	5

NA, not applicable; PE, paternal excess; ME, maternal excess.

[1], either paternal (PE) or maternal (ME) excess as defined in Scott et al., 1998. [2], determined by germination on soil. [3], counts done as described in Scott et al., 1998. [4], calculated relative to amount in 2x-2x control cross at heart stage (approx. 5 DAP). [5], expressed relative to 2x-2x control cross (usually 5 DAP). [6], measured as described in Scott et al., 1998. [7], seeds shriveled. [8], this experiment was performed ~~later~~ subsequent to the experiment that yielded the non-bracketed data and used improved growing techniques for the met1a/s plants. This resulted in more vigorous plants which presumably accounts for the observed changes in seed weight. Note however that the changes are qualitatively the same as the original experiment ~~i.e.,~~ i.e., 2x-2xmet are small than 2xmet-2xmet and 2xmet-2x are larger.

Please amend Table 3 at pp. **33-34** as follows:

	Outcome of Cross		
Cross	Endosperm Phenotype	Seed viability (%germination)	Hybrids formed?
4x*A. thaliana*X *A. lyrata*	ME	0	NO
4x*A. thaliana*Met1a/s X *A. lyrata*	Moderate PE	95-100	YES
4x*A. thaliana*X *C. arenosa*	Lethal PE	95-100	YES
2[4]x*A. thalianaX C. arenosa*	Lethal PE	0	NO
4x*A. thaliana*Met1a/s			

X *C. arenosa*	Lethal PE	0	NO

Please amend the paragraph beginning at page **34**, line **25** as follows:

In the absence of fertilization, *Arabidopsis* plants heterozygous for the *fie-1* mutation (*fie/FIE*) produce seeds with partial endosperm development (Ohad et al., 1996; 1999; see also ~~Table 3~~ Table 4 and Fig. 12 A-C). These 'autonomous' endosperms consist of a severely reduced number of endosperm nuclei (compared to wild type controls) and the endosperm fails to undergo cellularization. The seed collapses and becomes shriveled at maturity (Table 4). Consequently, the *fie* mutation conditions only limited endosperm development restricting its utility in the production of autonomous apomictic seed crops or embryoless seed crops. Endosperms produced in plants carrying the *fis1/mea* and *fis2* mutations are very similar to those of *fie/FIE* plants, and hence the utility of these genes is also restricted.

Please amend Table 4, at page **37** in the header for Seed weight as follows:

Table 4. Enhancement of endosperm development in *fie* mutant seeds by hypomethylation.

	Mature Seed phenotypes (%)[1]		Seed viability[2]		Seed weight (µg)[3]		Extent of endosperm development (%)[4]	
	Plump seeds	Shrivelled seeds	Plump seeds	Shrivelled seeds	Plum seeds	Shrivelled seeds	Complete	Partial
FIE/fie X 2x	50	50	95-100	0	25	15	50	50[5]
FIE/fie X 2xmet	100	0	95-100	NA	50%=15 50%=30	NA	100	0
FIE/fie emasculate	0	100	NA	0	NA	5	0	100[6]
FIE/fie: 2xmetHET emasculate	0	100	NA	0	NA	20	100	0